

SEQUENCE LISTING

<110> Reed, John C.
Matsuzawa, Shu-ichi

<120> Nucleic Acid Encoding Proteins Involved
in Protein Degradation, Products and Methods Related Thereto

<130> 66821-235

<150> US 09/591,694

<151> 2000-06-09

<160> 50

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1274

<212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (274)...(1167)

<400> 1

```
tttcttttagt tgtttatggg ccatttttcta ttttagcatt tattattcta tgtagtctat 60
ccaaagacga ttaagggagt tccacatggt ttccggaaca ttttgaaaag agagcttatac 120
cagtgtacag atcctaataa agtgcacatt cagtgttaatt ttattttttt aatatctttt 180
ttaatcctat ttttcttcct cttttgctca gtaaattttg tatgaaactt taaaaggact 240
tatggcatgt aaacattatt tataaagtaa gtc atg gtt ata att att ttt ctc 294
                                Met Val Ile Ile Ile Phe Leu
                                1                     5
```

```
ctg cct cct tat gta ttt att tca gaa atg agc cgt cag act gct aca 342
Leu Pro Pro Tyr Val Phe Ile Ser Glu Met Ser Arg Gln Thr Ala Thr
      10                     15                     20
```

```
gca tta cct acc ggt acc tcg aag tgt cca cca tcc cag agg gtg cct 390
Ala Leu Pro Thr Gly Thr Ser Lys Cys Pro Pro Ser Gln Arg Val Pro
      25                     30                     35
```

```
gcc ctg act ggc aca act gca tcc aac aat gac ttg gcg agt ctt ttt 438
Ala Leu Thr Gly Thr Thr Ala Ser Asn Asn Asp Leu Ala Ser Leu Phe
      40                     45                     50                     55
```

```
gag tgt cca gtc tgc ttt gac tat gtg tta ccg ccc att ctt caa tgt 486
Glu Cys Pro Val Cys Phe Asp Tyr Val Leu Pro Pro Ile Leu Gln Cys
      60                     65                     70
```

cag agt ggc cat ctt gtt tgt agc aac tgt cgc cca aag ctc aca tgt	534
Gln Ser Gly His Leu Val Cys Ser Asn Cys Arg Pro Lys Leu Thr Cys	
75 80 85	
tgt cca act tgc cgg ggc cct ttg gga tcc att cgc aac ttg gct atg	582
Cys Pro Thr Cys Arg Gly Pro Leu Gly Ser Ile Arg Asn Leu Ala Met	
90 95 100	
gag aaa gtg gct aat tca gta ctt ttc ccc tgt aaa tat gcg tct tct	630
Glu Lys Val Ala Asn Ser Val Leu Phe Pro Cys Lys Tyr Ala Ser Ser	
105 110 115	
gga tgt gaa ata act ctg cca cac aca gaa aaa gca gac cat gaa gag	678
Gly Cys Glu Ile Thr Leu Pro His Thr Glu Lys Ala Asp His Glu Glu	
120 125 130 135	
ctc tgt gag ttt agg cct tat tcc tgt ccg tgc cct ggt gct tcc tgt	726
Leu Cys Glu Phe Arg Pro Tyr Ser Cys Pro Cys Pro Gly Ala Ser Cys	
140 145 150	
aaa tgg caa ggc tct ctg gat gct gta atg ccc cat ctg atg cat cag	774
Lys Trp Gln Gly Ser Leu Asp Ala Val Met Pro His Leu Met His Gln	
155 160 165	
cat aag tcc att aca acc cta cag gga gag gat ata gtt ttt ctt gct	822
His Lys Ser Ile Thr Thr Leu Gln Gly Glu Asp Ile Val Phe Leu Ala	
170 175 180	
aca gac att aat ctt cct ggt gct gtt gac tgg gtg atg atg cag tcc	870
Thr Asp Ile Asn Leu Pro Gly Ala Val Asp Trp Val Met Met Gln Ser	
185 190 195	
tgt ttt ggc ttt cac ttc atg tta gtc tta gag aaa cag gaa aaa tac	918
Cys Phe Gly Phe His Phe Met Leu Val Leu Glu Lys Gln Glu Lys Tyr	
200 205 210 215	
gat ggt cac cag cag ttc ttc gca atc gta cag ctg ata gga aca cgc	966
Asp Gly His Gln Gln Phe Phe Ala Ile Val Gln Leu Ile Gly Thr Arg	
220 225 230	
aag caa gct gaa aat ttt gct tac cga ctt gag cta aat ggt cat agg	1014
Lys Gln Ala Glu Asn Phe Ala Tyr Arg Leu Glu Leu Asn Gly His Arg	
235 240 245	
cga cga ttg act tgg gaa gcg act cct cga tct att cat gaa gga att	1062
Arg Arg Leu Thr Trp Glu Ala Thr Pro Arg Ser Ile His Glu Gly Ile	
250 255 260	
gca aca gcc att atg aat agc gac tgt cta gtc ttt gac acc agc att	1110
Ala Thr Ala Ile Met Asn Ser Asp Cys Leu Val Phe Asp Thr Ser Ile	
265 270 275	
gca cag ctt ttt gca gaa aat ggc aat tta ggc atc aat gta act att	1158

Ala Gln Leu Phe Ala Glu Asn Gly Asn Leu Gly Ile Asn Val Thr Ile
280 285 290 295

tcc atg tgt tgaaatggca atcaaacatt ttctggccag tgttttaaacc 1207
Ser Met Cys

ttcagttttca cagaaaaataa ggcacccatc tgtctgccaa cctaaaaactc tttcggtagg 1267
tggaagc 1274

<210> 2
<211> 298
<212> PRT
<213> Homo sapien

<400> 2
Met Val Ile Ile Ile Phe Leu Leu Pro Pro Tyr Val Phe Ile Ser Glu
1 5 10 15
Met Ser Arg Gln Thr Ala Thr Ala Leu Pro Thr Gly Thr Ser Lys Cys
20 25 30
Pro Pro Ser Gln Arg Val Pro Ala Leu Thr Gly Thr Thr Ala Ser Asn
35 40 45
Asn Asp Leu Ala Ser Leu Phe Glu Cys Pro Val Cys Phe Asp Tyr Val
50 55 60
Leu Pro Pro Ile Leu Gln Cys Gln Ser Gly His Leu Val Cys Ser Asn
65 70 75 80
Cys Arg Pro Lys Leu Thr Cys Cys Pro Thr Cys Arg Gly Pro Leu Gly
85 90 95
Ser Ile Arg Asn Leu Ala Met Glu Lys Val Ala Asn Ser Val Leu Phe
100 105 110
Pro Cys Lys Tyr Ala Ser Ser Gly Cys Glu Ile Thr Leu Pro His Thr
115 120 125
Glu Lys Ala Asp His Glu Glu Leu Cys Glu Phe Arg Pro Tyr Ser Cys
130 135 140
Pro Cys Pro Gly Ala Ser Cys Lys Trp Gln Gly Ser Leu Asp Ala Val
145 150 155 160
Met Pro His Leu Met His Gln His Lys Ser Ile Thr Thr Leu Gln Gly
165 170 175
Glu Asp Ile Val Phe Leu Ala Thr Asp Ile Asn Leu Pro Gly Ala Val
180 185 190
Asp Trp Val Met Met Gln Ser Cys Phe Gly Phe His Phe Met Leu Val
195 200 205
Leu Glu Lys Gln Glu Lys Tyr Asp Gly His Gln Gln Phe Phe Ala Ile
210 215 220
Val Gln Leu Ile Gly Thr Arg Lys Gln Ala Glu Asn Phe Ala Tyr Arg
225 230 235 240
Leu Glu Leu Asn Gly His Arg Arg Arg Leu Thr Trp Glu Ala Thr Pro
245 250 255
Arg Ser Ile His Glu Gly Ile Ala Thr Ala Ile Met Asn Ser Asp Cys
260 265 270
Leu Val Phe Asp Thr Ser Ile Ala Gln Leu Phe Ala Glu Asn Gly Asn
275 280 285
Leu Gly Ile Asn Val Thr Ile Ser Met Cys

290

295

<210> 3
<211> 1432
<212> DNA
<213> Homo sapien

<220>
<221> CDS
<222> (25)...(708)

<400> 3
ggacttcggc ctgacccagc cccc atg gct tca gaa gag cta cag aaa gat 51
Met Ala Ser Glu Glu Leu Gln Lys Asp
1 5

cta gaa gag gta aag gtg ttg ctg gaa aag gct act agg aaa aga gta 99
Leu Glu Glu Val Lys Val Leu Leu Glu Lys Ala Thr Arg Lys Arg Val
10 15 20 25

cgt gat gcc ctt aca gct gaa aaa tcc aag att gag aca gaa atc aag 147
Arg Asp Ala Leu Thr Ala Glu Lys Ser Lys Ile Glu Thr Glu Ile Lys
30 35 40

aac aag atg caa cag aaa tca cag aag aaa gca gaa ctt ctt gat aat 195
Asn Lys Met Gln Gln Lys Ser Gln Lys Lys Ala Glu Leu Leu Asp Asn
45 50 55

gaa aaa cca gct gct gtg gtt gct ccc att aca acg ggc tat acg gtg 243
Glu Lys Pro Ala Ala Val Val Ala Pro Ile Thr Thr Gly Tyr Thr Val
60 65 70

aaa atc agt aat tat gga tgg gat cag tca gat aag ttt gtg aaa atc 291
Lys Ile Ser Asn Tyr Gly Trp Asp Gln Ser Asp Lys Phe Val Lys Ile
75 80 85

tac att acc tta act gga gtt cat caa gtt ccc act gag aat gtg cag 339
Tyr Ile Thr Leu Thr Gly Val His Gln Val Pro Thr Glu Asn Val Gln
90 95 100 105

gtg cat ttc aca gag agg tca ttt gat ctt ttg gta aag aat cta aat 387
Val His Phe Thr Glu Arg Ser Phe Asp Leu Leu Val Lys Asn Leu Asn
110 115 120

ggg aag agt tac tcc atg att gtg aac aat ctc ttg aaa ccc atc tct 435
Gly Lys Ser Tyr Ser Met Ile Val Asn Asn Leu Leu Lys Pro Ile Ser
125 130 135

gtg gaa ggc agt tca aaa aaa gtc aag act gat aca gtt ctt ata ttg 483
Val Glu Gly Ser Ser Lys Lys Val Lys Thr Asp Thr Val Leu Ile Leu
140 145 150

tgt aga aag aaa gtg gaa aac aca agg tgg gat tac ctg acc cag gtt 531
Cys Arg Lys Lys Val Glu Asn Thr Arg Trp Asp Tyr Leu Thr Gln Val
155 160 165

gaa aag gag tgc aaa gaa aaa gag aag ccc tcc tat gac act gaa aca 579
Glu Lys Glu Cys Lys Glu Lys Glu Lys Pro Ser Tyr Asp Thr Glu Thr
170 175 180 185

gat cct agt gag gga ttg atg aat gtt cta aag aaa att tat gaa gat 627
Asp Pro Ser Glu Gly Leu Met Asn Val Leu Lys Lys Ile Tyr Glu Asp
190 195 200

gga gac gat gat atg aag cga acc att aat aaa gcc tgg gtg gaa tca 675
Gly Asp Asp Asp Met Lys Arg Thr Ile Asn Lys Ala Trp Val Glu Ser
205 210 215

aga gag aag caa gcc aaa gga gac acg gaa ttt tgagacttta aagtcgtttt 728
Arg Glu Lys Gln Ala Lys Gly Asp Thr Glu Phe
220 225

gggaactgtg atgtgatgtg gaaatactga tgtttccagt aagggaatat tgggtgagctg 788
catatataaaa tttgacagat agctatttac atagccttct aagtaaaggc aatgaattct 848
ccatttccta ctggaggatt tatttaaata aaatatgctt attaaacact cctgcaaaga 908
tgggttttatt agtaccctgg tcattttgtt caaggaaggg ttatatgca ttctcacgtg 968
aaatataaaa agcaagtctt gcccaataaa aacgctacat tgtgtgtatt ttttgttcag 1028
ctaagaattg gaaaagtatt tgcttgccct ttaagttact gacatcagct tccaccagt 1088
taaaaattga gtaaaacctg aagttttgca taaaatgcaa atcgggtgcct gtgcttgaag 1148
gttgctgtag agcatctgac cccttattac caccttaagc aatgtatatg ccatgcatta 1208
ccatgcacta attcaatcac aggtgtttct atctagattt aaatatattt gtcaatgaat 1268
gtggaataga aaatctaaac atgacaataa tagacatata tttgtatggg accagttagt 1328
tttgccgtgg atcagatggg ttataaaagt aataaccata aagcaaaaaa taatttgaaa 1388
gcccgctctat tcctatgctc aataaagtta agtttttctt catt 1432

<210> 4

<211> 228

<212> PRT

<213> Homo sapien

<400> 4

Met Ala Ser Glu Glu Leu Gln Lys Asp Leu Glu Glu Val Lys Val Leu
1 5 10 15
Leu Glu Lys Ala Thr Arg Lys Arg Val Arg Asp Ala Leu Thr Ala Glu
20 25 30
Lys Ser Lys Ile Glu Thr Glu Ile Lys Asn Lys Met Gln Gln Lys Ser
35 40 45
Gln Lys Lys Ala Glu Leu Leu Asp Asn Glu Lys Pro Ala Ala Val Val
50 55 60
Ala Pro Ile Thr Thr Gly Tyr Thr Val Lys Ile Ser Asn Tyr Gly Trp
65 70 75 80
Asp Gln Ser Asp Lys Phe Val Lys Ile Tyr Ile Thr Leu Thr Gly Val
85 90 95
His Gln Val Pro Thr Glu Asn Val Gln Val His Phe Thr Glu Arg Ser
100 105 110

Phe	Asp	Leu	Leu	Val	Lys	Asn	Leu	Asn	Gly	Lys	Ser	Tyr	Ser	Met	Ile
	115						120				125				
Val	Asn	Asn	Leu	Leu	Lys	Pro	Ile	Ser	Val	Glu	Gly	Ser	Ser	Lys	Lys
	130					135				140					
Val	Lys	Thr	Asp	Thr	Val	Leu	Ile	Leu	Cys	Arg	Lys	Lys	Val	Glu	Asn
145					150				155					160	
Thr	Arg	Trp	Asp	Tyr	Leu	Thr	Gln	Val	Glu	Lys	Glu	Cys	Lys	Glu	Lys
			165						170					175	
Glu	Lys	Pro	Ser	Tyr	Asp	Thr	Glu	Thr	Asp	Pro	Ser	Glu	Gly	Leu	Met
		180					185						190		
Asn	Val	Leu	Lys	Lys	Ile	Tyr	Glu	Asp	Gly	Asp	Asp	Asp	Met	Lys	Arg
	195						200					205			
Thr	Ile	Asn	Lys	Ala	Trp	Val	Glu	Ser	Arg	Glu	Lys	Gln	Ala	Lys	Gly
	210					215					220				
Asp	Thr	Glu	Phe												
225															

<210> 5
 <211> 1413
 <212> DNA
 <213> Homo sapien

<220>
 <221> CDS
 <222> (25) ... (264)

<400> 5
 ggacttcgggc ctgacccagc cccc atg gct tca gaa gag cta cag aaa gat 51
 Met Ala Ser Glu Glu Leu Gln Lys Asp
 1 5

cta gaa gag gta aag gtg ttg ctg gaa aag gct act agg aaa aga gta 99
 Leu Glu Glu Val Lys Val Leu Leu Glu Lys Ala Thr Arg Lys Arg Val
 10 15 20 25

cgt gat gcc ctt aca gct gaa aaa tcc aag att gag aca gaa atc aag 147
 Arg Asp Ala Leu Thr Ala Glu Lys Ser Lys Ile Glu Thr Glu Ile Lys
 30 35 40

aac aag atg caa cag aaa tca cag aag aaa gca gaa ctt ctt gat aat 195
 Asn Lys Met Gln Gln Lys Ser Gln Lys Lys Ala Glu Leu Leu Asp Asn
 45 50 55

gaa aaa cca gct gct gtg gtt gct ccc att aca acg ggc tat acg gat 243
 Glu Lys Pro Ala Ala Val Val Ala Pro Ile Thr Thr Gly Tyr Thr Asp
 60 65 70

ggg atc agt cag ata agt ttg tgaaaatcta cattacctta actggagttc 294
 Gly Ile Ser Gln Ile Ser Leu
 75 80

atcaagttcc cactgagaat gtgcaggtgc atttcacaga gaggtcattt gatcttttgg 354

```

taaagaatct aaatgggaag agttactcca tgattgtgaa caatctcttg aaacccatct 414
ctgtggaagg cagttcaaaa aaagtcaaga ctgatacagt tcttatattg tgtagaaaaga 474
aagtggaaaa cacaagggtg gattacctga cccagggtga aaaggagtgc aaagaaaaag 534
agaagccctc ctatgacact gaaacagatc ctagtgaggg attgatgaat gttctaaaga 594
aaatttatga agatggagac gatgatatga agcgaacat taataaagcc tgggtggaat 654
caagagagaa gcaagccaaa ggagacacgg aattttgaga ctttaaagtc gttttgggaa 714
ctgtgatgtg atgtggaaat actgatgttt ccagtaaggg aatattggtg agctgcatat 774
ataaatttga cagatagcta ttacatagc cttctaagta aaggcaatga attctccatt 834
tcctactgga ggatttattt aaataaaata tgcttattaa aactcctgc aaagatgggt 894
ttattagtac cctggtcatt ttgttcaagg aagggttata ttgcattctc acgtgaaata 954
taaaaagcaa gtcttgccca ataaaaacgc tacatttgtt gtattttttg ttcagctaag 1014
aattggaaaa gtatttgctt gccttttaag ttactgacat cagcttcac cagtgtaaaa 1074
attgagtaaa acctgaagtt ttgcataaaa tgcaaacgg tgctgtgtc tgaagggtgc 1134
tgtagagcat ctgaccctt attaccacct taagcaatgt atatgccatg cattaccatg 1194
cactaattca atcacaggtg tttctatcta gatttaaata tatttgtcaa tgaatgtgga 1254
atagaaaatc taaacatgac aataatagac atatctttgt atggtaccag ttagttttgc 1314
cgtggatcag atggtttata aaagtaataa ccataaagca aaaaataatt tgaaagcccg 1374
tctattccta tgctcaataa agttaagttt ttcttcatt 1413

```

<210> 6

<211> 80

<212> PRT

<213> Homo sapien

<400> 6

```

Met Ala Ser Glu Glu Leu Gln Lys Asp Leu Glu Glu Val Lys Val Leu
 1             5             10             15
Leu Glu Lys Ala Thr Arg Lys Arg Val Arg Asp Ala Leu Thr Ala Glu
      20             25             30
Lys Ser Lys Ile Glu Thr Glu Ile Lys Asn Lys Met Gln Gln Lys Ser
      35             40             45
Gln Lys Lys Ala Glu Leu Leu Asp Asn Glu Lys Pro Ala Ala Val Val
      50             55             60
Ala Pro Ile Thr Thr Gly Tyr Thr Asp Gly Ile Ser Gln Ile Ser Leu
65             70             75             80

```

<210> 7

<211> 1673

<212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (61)...(1389)

<400> 7

```

ccggagggtg caggcgacgg gaagcgcggtg tggtcggctg gggtcggct cctggagaac 60
atg gcc cgg cct ccc ggg ggc tct ggt ccc ctc ctc gat tca gag cat 108
Met Ala Arg Pro Pro Gly Gly Ser Gly Pro Leu Leu Asp Ser Glu His
 1             5             10             15

tct tca ctc cag aat aat gag caa ccc tct ttg gcc acc agc tcc aat 156

```

Ser	Ser	Leu	Gln	Asn	Asn	Glu	Gln	Pro	Ser	Leu	Ala	Thr	Ser	Ser	Asn		
			20					25					30				
cag	act	agc	atg	cag	gat	gaa	caa	cca	agt	gat	tca	ttc	caa	gga	cag	204	
Gln	Thr	Ser	Met	Gln	Asp	Glu	Gln	Pro	Ser	Asp	Ser	Phe	Gln	Gly	Gln		
		35					40					45					
gca	gcc	cag	tct	ggg	gtt	tgg	aat	gac	gac	agt	atg	tta	ggg	cct	agt	252	
Ala	Ala	Gln	Ser	Gly	Val	Trp	Asn	Asp	Asp	Ser	Met	Leu	Gly	Pro	Ser		
		50				55					60						
caa	aat	ttt	gaa	gct	gag	tca	att	caa	gat	aat	gcg	cat	atg	gca	gag	300	
Gln	Asn	Phe	Glu	Ala	Glu	Ser	Ile	Gln	Asp	Asn	Ala	His	Met	Ala	Glu		
		65				70				75					80		
ggc	aca	ggg	ttc	tat	ccc	tca	gaa	ccc	atg	ctc	tgt	agt	gaa	tcg	gtg	348	
Gly	Thr	Gly	Phe	Tyr	Pro	Ser	Glu	Pro	Met	Leu	Cys	Ser	Glu	Ser	Val		
				85					90					95			
gaa	ggg	caa	gtg	cca	cat	tca	tta	gag	acc	ttg	tat	caa	tca	gct	gac	396	
Glu	Gly	Gln	Val	Pro	His	Ser	Leu	Glu	Thr	Leu	Tyr	Gln	Ser	Ala	Asp		
			100					105					110				
tgt	tct	gat	gcc	aat	gat	gcc	ttg	ata	gtg	ttg	ata	cat	ctt	ctc	atg	444	
Cys	Ser	Asp	Ala	Asn	Asp	Ala	Leu	Ile	Val	Leu	Ile	His	Leu	Leu	Met		
			115				120					125					
ttg	gag	tca	ggg	tac	ata	cct	cag	ggc	acc	gaa	gcc	aaa	gca	ctg	tcc	492	
Leu	Glu	Ser	Gly	Tyr	Ile	Pro	Gln	Gly	Thr	Glu	Ala	Lys	Ala	Leu	Ser		
		130				135					140						
atg	ccg	gag	aag	tgg	aag	ttg	agc	ggg	gtg	tat	aag	ctg	cag	tac	atg	540	
Met	Pro	Glu	Lys	Trp	Lys	Leu	Ser	Gly	Val	Tyr	Lys	Leu	Gln	Tyr	Met		
		145			150				155					160			
cat	cct	ctc	tgc	gag	ggc	agc	tcc	gct	act	ctc	acc	tgt	gtg	cct	ttg	588	
His	Pro	Leu	Cys	Glu	Gly	Ser	Ser	Ala	Thr	Leu	Thr	Cys	Val	Pro	Leu		
			165					170					175				
gga	aac	ctg	att	gtt	gta	aat	gct	aca	cta	aaa	atc	aac	aat	gag	att	636	
Gly	Asn	Leu	Ile	Val	Val	Asn	Ala	Thr	Leu	Lys	Ile	Asn	Asn	Glu	Ile		
			180				185					190					
aga	agt	gtg	aaa	aga	ttg	cag	ctg	cta	cca	aaa	tct	ttt	att	tgc	aaa	684	
Arg	Ser	Val	Lys	Arg	Leu	Gln	Leu	Leu	Pro	Lys	Ser	Phe	Ile	Cys	Lys		
		195				200						205					
gag	aaa	cta	ggg	gaa	aat	gta	gcc	aac	ata	tac	aaa	gat	ctt	cag	aaa	732	
Glu	Lys	Leu	Gly	Glu	Asn	Val	Ala	Asn	Ile	Tyr	Lys	Asp	Leu	Gln	Lys		
		210				215					220						
ctc	tct	cgc	ctc	ttt	aaa	gac	cag	ctg	gtg	tat	cct	ctt	ctg	gct	ttt	780	
Leu	Ser	Arg	Leu	Phe	Lys	Asp	Gln	Leu	Val	Tyr	Pro	Leu	Leu	Ala	Phe		

225	230	235	240	
acc cga caa gca ctg aac cta cca gat gta ttt ggg ttg gtc gtc ctc	828			
Thr Arg Gln Ala Leu Asn Leu Pro Asp Val Phe Gly Leu Val Val Leu				
245	250	255		
cca ttg gaa ctg aaa cta cgg atc ttc cga ctt ctg gat gtt cgt tcc	876			
Pro Leu Glu Leu Lys Leu Arg Ile Phe Arg Leu Leu Asp Val Arg Ser				
260	265	270		
gtc ttg tct ttg tct gcg gtt tgt cgt gac ctc ttt act gct tca aat	924			
Val Leu Ser Leu Ser Ala Val Cys Arg Asp Leu Phe Thr Ala Ser Asn				
275	280	285		
gac cca ctc ctg tgg agg ttt tta tat ctg cgt gat ttt cga gac aat	972			
Asp Pro Leu Leu Trp Arg Phe Leu Tyr Leu Arg Asp Phe Arg Asp Asn				
290	295	300		
act gtc aga gtt caa gac aca gat tgg aaa gaa ctg tac agg aag agg	1020			
Thr Val Arg Val Gln Asp Thr Asp Trp Lys Glu Leu Tyr Arg Lys Arg				
305	310	315	320	
cac ata caa aga aaa gaa tcc ccg aaa ggg cgg ttt gtg atg ctc ctg	1068			
His Ile Gln Arg Lys Glu Ser Pro Lys Gly Arg Phe Val Met Leu Leu				
325	330	335		
cca tcg tca act cac acc att cca ttc tat ccc aac ccc ttg cac cct	1116			
Pro Ser Ser Thr His Thr Ile Pro Phe Tyr Pro Asn Pro Leu His Pro				
340	345	350		
agg cca ttt cct agc tcc cgc ctt cct cca gga att atc ggg ggt gaa	1164			
Arg Pro Phe Pro Ser Ser Arg Leu Pro Pro Gly Ile Ile Gly Gly Glu				
355	360	365		
tat gac caa aga cca aca ctt ccc tat gtt gga gac cca atc agt tca	1212			
Tyr Asp Gln Arg Pro Thr Leu Pro Tyr Val Gly Asp Pro Ile Ser Ser				
370	375	380		
ctc att cct ggt cct ggg gag acg ccc agc cag ttt cct cca ctg aga	1260			
Leu Ile Pro Gly Pro Gly Glu Thr Pro Ser Gln Phe Pro Pro Leu Arg				
385	390	395	400	
cca cgc ttt gat cca gtt ggc cca ctt cca gga cct aac ccc atc ttg	1308			
Pro Arg Phe Asp Pro Val Gly Pro Leu Pro Gly Pro Asn Pro Ile Leu				
405	410	415		
cca ggg cga ggc ggc ccc aat gac aga ttt ccc ttt aga ccc agc agg	1356			
Pro Gly Arg Gly Gly Pro Asn Asp Arg Phe Pro Phe Arg Pro Ser Arg				
420	425	430		
ggg cgg cca act gat ggc cgg ctg tca ttc atg tgattgattt gtaatttc	1409			
Gly Arg Pro Thr Asp Gly Arg Leu Ser Phe Met				
435	440			

```

ttctggagct ccatttgttt ttgtttctaa actacagatg tcaactcctt ggggtgctga 1469
tctcgagtgt tatttttctga ttgtggtggt gagagttgca ctcccagaaa ccttttaaga 1529
gatacattta tagccctagg ggtggtatga cccaaaggtt cctctgtgac aaggttggcc 1589
ttgggaatag ttggctgcca atctccctgc tcttggttct cctctagatt gaagtttgtt 1649
ttctgatgct gttcttacca gatt                                     1673

```

<210> 8

<211> 443

<212> PRT

<213> Homo sapien

<400> 8

```

Met Ala Arg Pro Pro Gly Gly Ser Gly Pro Leu Leu Asp Ser Glu His
 1           5           10           15
Ser Ser Leu Gln Asn Asn Glu Gln Pro Ser Leu Ala Thr Ser Ser Asn
      20           25           30
Gln Thr Ser Met Gln Asp Glu Gln Pro Ser Asp Ser Phe Gln Gly Gln
      35           40           45
Ala Ala Gln Ser Gly Val Trp Asn Asp Asp Ser Met Leu Gly Pro Ser
      50           55           60
Gln Asn Phe Glu Ala Glu Ser Ile Gln Asp Asn Ala His Met Ala Glu
65           70           75           80
Gly Thr Gly Phe Tyr Pro Ser Glu Pro Met Leu Cys Ser Glu Ser Val
      85           90           95
Glu Gly Gln Val Pro His Ser Leu Glu Thr Leu Tyr Gln Ser Ala Asp
      100          105          110
Cys Ser Asp Ala Asn Asp Ala Leu Ile Val Leu Ile His Leu Leu Met
      115          120          125
Leu Glu Ser Gly Tyr Ile Pro Gln Gly Thr Glu Ala Lys Ala Leu Ser
      130          135          140
Met Pro Glu Lys Trp Lys Leu Ser Gly Val Tyr Lys Leu Gln Tyr Met
145          150          155          160
His Pro Leu Cys Glu Gly Ser Ser Ala Thr Leu Thr Cys Val Pro Leu
      165          170          175
Gly Asn Leu Ile Val Val Asn Ala Thr Leu Lys Ile Asn Asn Glu Ile
      180          185          190
Arg Ser Val Lys Arg Leu Gln Leu Leu Pro Lys Ser Phe Ile Cys Lys
      195          200          205
Glu Lys Leu Gly Glu Asn Val Ala Asn Ile Tyr Lys Asp Leu Gln Lys
      210          215          220
Leu Ser Arg Leu Phe Lys Asp Gln Leu Val Tyr Pro Leu Leu Ala Phe
225          230          235          240
Thr Arg Gln Ala Leu Asn Leu Pro Asp Val Phe Gly Leu Val Val Leu
      245          250          255
Pro Leu Glu Leu Lys Leu Arg Ile Phe Arg Leu Leu Asp Val Arg Ser
      260          265          270
Val Leu Ser Leu Ser Ala Val Cys Arg Asp Leu Phe Thr Ala Ser Asn
      275          280          285
Asp Pro Leu Leu Trp Arg Phe Leu Tyr Leu Arg Asp Phe Arg Asp Asn
      290          295          300
Thr Val Arg Val Gln Asp Thr Asp Trp Lys Glu Leu Tyr Arg Lys Arg
305          310          315          320

```

His	Ile	Gln	Arg	Lys	Glu	Ser	Pro	Lys	Gly	Arg	Phe	Val	Met	Leu	Leu
				325					330					335	
Pro	Ser	Ser	Thr	His	Thr	Ile	Pro	Phe	Tyr	Pro	Asn	Pro	Leu	His	Pro
			340					345					350		
Arg	Pro	Phe	Pro	Ser	Ser	Arg	Leu	Pro	Pro	Gly	Ile	Ile	Gly	Gly	Glu
		355					360						365		
Tyr	Asp	Gln	Arg	Pro	Thr	Leu	Pro	Tyr	Val	Gly	Asp	Pro	Ile	Ser	Ser
	370					375					380				
Leu	Ile	Pro	Gly	Pro	Gly	Glu	Thr	Pro	Ser	Gln	Phe	Pro	Pro	Leu	Arg
385						390				395					400
Pro	Arg	Phe	Asp	Pro	Val	Gly	Pro	Leu	Pro	Gly	Pro	Asn	Pro	Ile	Leu
			405						410					415	
Pro	Gly	Arg	Gly	Pro	Asn	Asp	Arg	Phe	Pro	Phe	Arg	Pro	Ser	Arg	
		420					425					430			
Gly	Arg	Pro	Thr	Asp	Gly	Arg	Leu	Ser	Phe	Met					
		435					440								

<210> 9

<211> 1892

<212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (43)...(1608)

<400> 9

gccgcttcgcg	gggccaggcc	cctcgggccg	cctgcccgcg	tc	atg	agg	ctg	cgg		54
					Met	Arg	Leu	Arg		
					1					

gtg	cgg	ctt	ctg	aag	cgg	acc	tgg	ccg	ctg	gag	gtg	ccc	gag	acg	gag	102
Val	Arg	Leu	Leu	Lys	Arg	Thr	Trp	Pro	Leu	Glu	Val	Pro	Glu	Thr	Glu	
5					10				15					20		

ccg	acg	ctg	ggg	cat	ttg	cgc	tcg	cac	ctg	agg	cag	tcc	ctg	ctg	tgc	150
Pro	Thr	Leu	Gly	His	Leu	Arg	Ser	His	Leu	Arg	Gln	Ser	Leu	Leu	Cys	
				25				30						35		

acc	tgg	ggg	tac	agt	tct	aat	acc	cga	ttt	aca	att	aca	ttg	aac	tac	198
Thr	Trp	Gly	Tyr	Ser	Ser	Asn	Thr	Arg	Phe	Thr	Ile	Thr	Leu	Asn	Tyr	
			40				45						50			

aag	gat	ccc	ctc	act	gga	gat	gaa	gag	acc	ttg	gct	tca	tat	ggg	att	246
Lys	Asp	Pro	Leu	Thr	Gly	Asp	Glu	Glu	Thr	Leu	Ala	Ser	Tyr	Gly	Ile	
		55					60					65				

gtt	tct	ggg	gac	ttg	ata	tgt	ttg	att	ctt	caa	gat	gac	att	cca	gcg	294
Val	Ser	Gly	Asp	Leu	Ile	Cys	Leu	Ile	Leu	Gln	Asp	Asp	Ile	Pro	Ala	
	70					75				80						

cct	aat	ata	cct	tca	tcc	aca	gat	tca	gag	cat	tct	tca	ctc	cag	aat	342
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Pro	Asn	Ile	Pro	Ser	Ser	Thr	Asp	Ser	Glu	His	Ser	Ser	Leu	Gln	Asn		
85					90					95					100		
aat	gag	caa	ccc	tct	ttg	gcc	acc	agc	tcc	aat	cag	act	agc	atg	cag	390	
Asn	Glu	Gln	Pro	Ser	Leu	Ala	Thr	Ser	Ser	Asn	Gln	Thr	Ser	Met	Gln		
				105					110					115			
gat	gaa	caa	cca	agt	gat	tca	ttc	caa	gga	cag	gca	gcc	cag	tct	ggc	438	
Asp	Glu	Gln	Pro	Ser	Asp	Ser	Phe	Gln	Gly	Gln	Ala	Ala	Gln	Ser	Gly		
			120					125					130				
gtt	tgg	aat	gac	gac	agt	atg	tta	ggg	cct	agt	caa	aat	ttt	gaa	gct	486	
Val	Trp	Asn	Asp	Asp	Ser	Met	Leu	Gly	Pro	Ser	Gln	Asn	Phe	Glu	Ala		
		135					140					145					
gag	tca	att	caa	gat	aat	gcg	cat	atg	gca	gag	ggc	aca	ggc	ttc	tat	534	
Glu	Ser	Ile	Gln	Asp	Asn	Ala	His	Met	Ala	Glu	Gly	Thr	Gly	Phe	Tyr		
	150					155					160						
ccc	tca	gaa	ccc	atg	ctc	tgt	agt	gaa	tcg	gtg	gaa	ggg	caa	gtg	cca	582	
Pro	Ser	Glu	Pro	Met	Leu	Cys	Ser	Glu	Ser	Val	Glu	Gly	Gln	Val	Pro		
165					170					175					180		
cat	tca	tta	gag	acc	ttg	tat	caa	tca	gct	gac	tgt	tct	gat	gcc	aat	630	
His	Ser	Leu	Glu	Thr	Leu	Tyr	Gln	Ser	Ala	Asp	Cys	Ser	Asp	Ala	Asn		
				185					190					195			
gat	gcc	ttg	ata	gtg	ttg	ata	cat	ctt	ctc	atg	ttg	gag	tca	ggc	tac	678	
Asp	Ala	Leu	Ile	Val	Leu	Ile	His	Leu	Leu	Met	Leu	Glu	Ser	Gly	Tyr		
		200						205					210				
ata	cct	cag	ggc	acc	gaa	gcc	aaa	gca	ctg	tcc	atg	ccg	gag	aag	tgg	726	
Ile	Pro	Gln	Gly	Thr	Glu	Ala	Lys	Ala	Leu	Ser	Met	Pro	Glu	Lys	Trp		
		215					220					225					
aag	ttg	agc	ggg	gtg	tat	aag	ctg	cag	tac	atg	cat	cct	ctc	tgc	gag	774	
Lys	Leu	Ser	Gly	Val	Tyr	Lys	Leu	Gln	Tyr	Met	His	Pro	Leu	Cys	Glu		
	230					235					240						
ggc	agc	tcc	gct	act	ctc	acc	tgt	gtg	cct	ttg	gga	aac	ctg	att	gtt	822	
Gly	Ser	Ser	Ala	Thr	Leu	Thr	Cys	Val	Pro	Leu	Gly	Asn	Leu	Ile	Val		
245					250					255					260		
gta	aat	gct	aca	cta	aaa	atc	aac	aat	gag	att	aga	agt	gtg	aaa	aga	870	
Val	Asn	Ala	Thr	Leu	Lys	Ile	Asn	Asn	Glu	Ile	Arg	Ser	Val	Lys	Arg		
				265					270					275			
ttg	cag	ctg	cta	cca	aaa	tct	ttt	att	tgc	aaa	gag	aaa	cta	ggg	gaa	918	
Leu	Gln	Leu	Leu	Pro	Lys	Ser	Phe	Ile	Cys	Lys	Glu	Lys	Leu	Gly	Glu		
			280					285					290				
aat	gta	gcc	aac	ata	tac	aaa	gat	ctt	cag	aaa	ctc	tct	cgc	ctc	ttt	966	
Asn	Val	Ala	Asn	Ile	Tyr	Lys	Asp	Leu	Gln	Lys	Leu	Ser	Arg	Leu	Phe		

295	300	305	
aaa gac cag ctg gtg tat cct ctt ctg gct ttt acc cga caa gca ctg			1014
Lys Asp Gln Leu Val Tyr Pro Leu Leu Ala Phe Thr Arg Gln Ala Leu			
310	315	320	
aac cta cca gat gta ttt ggg ttg gtc gtc ctc cca ttg gaa ctg aaa			1062
Asn Leu Pro Asp Val Phe Gly Leu Val Val Leu Pro Leu Glu Leu Lys			
325	330	335	340
cta cgg atc ttc cga ctt ctg gat gtt cgt tcc gtc ttg tct ttg tct			1110
Leu Arg Ile Phe Arg Leu Leu Asp Val Arg Ser Val Leu Ser Leu Ser			
	345	350	355
gcg gtt tgt cgt gac ctc ttt act gct tca aat gac cca ctc ctg tgg			1158
Ala Val Cys Arg Asp Leu Phe Thr Ala Ser Asn Asp Pro Leu Leu Trp			
	360	365	370
agg ttt tta tat ctg cgt gat ttt cga gac aat act gtc aga gtt caa			1206
Arg Phe Leu Tyr Leu Arg Asp Phe Arg Asp Asn Thr Val Arg Val Gln			
	375	380	385
gac aca gat tgg aaa gaa ctg tac agg aag agg cac ata caa aga aaa			1254
Asp Thr Asp Trp Lys Glu Leu Tyr Arg Lys Arg His Ile Gln Arg Lys			
	390	395	400
gaa tcc ccg aaa ggg cgg ttt gtg atg ctc ctg cca tcg tca act cac			1302
Glu Ser Pro Lys Gly Arg Phe Val Met Leu Leu Pro Ser Ser Thr His			
405	410	415	420
acc att cca ttc tat ccc aac ccc ttg cac cct agg cca ttt cct agc			1350
Thr Ile Pro Phe Tyr Pro Asn Pro Leu His Pro Arg Pro Phe Pro Ser			
	425	430	435
tcc cgc ctt cct cca gga att atc ggg ggt gaa tat gac caa aga cca			1398
Ser Arg Leu Pro Pro Gly Ile Ile Gly Gly Glu Tyr Asp Gln Arg Pro			
	440	445	450
aca ctt ccc tat gtt gga gac cca atc agt tca ctc att cct ggt cct			1446
Thr Leu Pro Tyr Val Gly Asp Pro Ile Ser Ser Leu Ile Pro Gly Pro			
	455	460	465
ggg gag acg ccc agc cag ttt cct cca ctg aga cca cgc ttt gat cca			1494
Gly Glu Thr Pro Ser Gln Phe Pro Pro Leu Arg Pro Arg Phe Asp Pro			
	470	475	480
gtt ggc cca ctt cca gga cct aac ccc atc ttg cca ggg cga ggc ggc			1542
Val Gly Pro Leu Pro Gly Pro Asn Pro Ile Leu Pro Gly Arg Gly Gly			
485	490	495	500
ccc aat gac aga ttt ccc ttt aga ccc agc agg ggt cgg cca act gat			1590
Pro Asn Asp Arg Phe Pro Phe Arg Pro Ser Arg Gly Arg Pro Thr Asp			
	505	510	515

ggc cgg ctg tca ttc atg tgattgattt gtaatttcat ttctggagct 1638
Gly Arg Leu Ser Phe Met
520

ccatttgttt ttgtttctaa actacagatg tcaactcctt ggggtgctga tctcgagtgt 1698
tattttctga ttgtggtgtt gagagttgca ctcccagaaa ccttttaaga gatacattta 1758
tagccctagg ggtggtatga cccaaagggtt cctctgtgac aaggttggcc ttgggaatag 1818
ttggctgcc aatctcctgc tcttggttct cctctagatt gaagtttgtt ttctgatgct 1878
gttcttacca gatt 1892

<210> 10
<211> 522
<212> PRT
<213> Homo sapien

<400> 10
Met Arg Leu Arg Val Arg Leu Leu Lys Arg Thr Trp Pro Leu Glu Val
1 5 10 15
Pro Glu Thr Glu Pro Thr Leu Gly His Leu Arg Ser His Leu Arg Gln
20 25 30
Ser Leu Leu Cys Thr Trp Gly Tyr Ser Ser Asn Thr Arg Phe Thr Ile
35 40 45
Thr Leu Asn Tyr Lys Asp Pro Leu Thr Gly Asp Glu Glu Thr Leu Ala
50 55 60
Ser Tyr Gly Ile Val Ser Gly Asp Leu Ile Cys Leu Ile Leu Gln Asp
65 70 75 80
Asp Ile Pro Ala Pro Asn Ile Pro Ser Ser Thr Asp Ser Glu His Ser
85 90 95
Ser Leu Gln Asn Asn Glu Gln Pro Ser Leu Ala Thr Ser Ser Asn Gln
100 105 110
Thr Ser Met Gln Asp Glu Gln Pro Ser Asp Ser Phe Gln Gly Gln Ala
115 120 125
Ala Gln Ser Gly Val Trp Asn Asp Asp Ser Met Leu Gly Pro Ser Gln
130 135 140
Asn Phe Glu Ala Glu Ser Ile Gln Asp Asn Ala His Met Ala Glu Gly
145 150 155 160
Thr Gly Phe Tyr Pro Ser Glu Pro Met Leu Cys Ser Glu Ser Val Glu
165 170 175
Gly Gln Val Pro His Ser Leu Glu Thr Leu Tyr Gln Ser Ala Asp Cys
180 185 190
Ser Asp Ala Asn Asp Ala Leu Ile Val Leu Ile His Leu Leu Met Leu
195 200 205
Glu Ser Gly Tyr Ile Pro Gln Gly Thr Glu Ala Lys Ala Leu Ser Met
210 215 220
Pro Glu Lys Trp Lys Leu Ser Gly Val Tyr Lys Leu Gln Tyr Met His
225 230 235 240
Pro Leu Cys Glu Gly Ser Ser Ala Thr Leu Thr Cys Val Pro Leu Gly
245 250 255
Asn Leu Ile Val Val Asn Ala Thr Leu Lys Ile Asn Asn Glu Ile Arg
260 265 270
Ser Val Lys Arg Leu Gln Leu Leu Pro Lys Ser Phe Ile Cys Lys Glu
275 280 285

Lys	Leu	Gly	Glu	Asn	Val	Ala	Asn	Ile	Tyr	Lys	Asp	Leu	Gln	Lys	Leu
290						295				300					
Ser	Arg	Leu	Phe	Lys	Asp	Gln	Leu	Val	Tyr	Pro	Leu	Leu	Ala	Phe	Thr
305				310					315						320
Arg	Gln	Ala	Leu	Asn	Leu	Pro	Asp	Val	Phe	Gly	Leu	Val	Val	Leu	Pro
				325					330					335	
Leu	Glu	Leu	Lys	Leu	Arg	Ile	Phe	Arg	Leu	Leu	Asp	Val	Arg	Ser	Val
			340					345					350		
Leu	Ser	Leu	Ser	Ala	Val	Cys	Arg	Asp	Leu	Phe	Thr	Ala	Ser	Asn	Asp
		355					360					365			
Pro	Leu	Leu	Trp	Arg	Phe	Leu	Tyr	Leu	Arg	Asp	Phe	Arg	Asp	Asn	Thr
370						375					380				
Val	Arg	Val	Gln	Asp	Thr	Asp	Trp	Lys	Glu	Leu	Tyr	Arg	Lys	Arg	His
385				390					395						400
Ile	Gln	Arg	Lys	Glu	Ser	Pro	Lys	Gly	Arg	Phe	Val	Met	Leu	Leu	Pro
				405				410						415	
Ser	Ser	Thr	His	Thr	Ile	Pro	Phe	Tyr	Pro	Asn	Pro	Leu	His	Pro	Arg
			420					425					430		
Pro	Phe	Pro	Ser	Ser	Arg	Leu	Pro	Pro	Gly	Ile	Ile	Gly	Gly	Glu	Tyr
		435					440					445			
Asp	Gln	Arg	Pro	Thr	Leu	Pro	Tyr	Val	Gly	Asp	Pro	Ile	Ser	Ser	Leu
	450					455					460				
Ile	Pro	Gly	Pro	Gly	Glu	Thr	Pro	Ser	Gln	Phe	Pro	Pro	Leu	Arg	Pro
465					470					475					480
Arg	Phe	Asp	Pro	Val	Gly	Pro	Leu	Pro	Gly	Pro	Asn	Pro	Ile	Leu	Pro
				485					490					495	
Gly	Arg	Gly	Gly	Pro	Asn	Asp	Arg	Phe	Pro	Phe	Arg	Pro	Ser	Arg	Gly
			500					505					510		
Arg	Pro	Thr	Asp	Gly	Arg	Leu	Ser	Phe	Met						
		515					520								

<210> 11
 <211> 1075
 <212> DNA
 <213> Homo sapien

<220>
 <221> CDS
 <222> (52)...(1032)

<400> 11
 gctaatttag ctttatttct tcttttagcc atcaagtttt atcgtagggc t atg caa 57
 Met Gln
 1

ctt gta cct gat ata gag ttc aag att act tat acc cgg tct cca gat 105
 Leu Val Pro Asp Ile Glu Phe Lys Ile Thr Tyr Thr Arg Ser Pro Asp
 5 10 15

ggt gat ggc gtt gga aac agc tac att gaa gat aat gat gat gac agc 153
 Gly Asp Gly Val Gly Asn Ser Tyr Ile Glu Asp Asn Asp Asp Asp Ser
 20 25 30

aaa atg gca gat ctc ttg tcc tac ttc cag cag caa ctc aca ttt cag	201
Lys Met Ala Asp Leu Leu Ser Tyr Phe Gln Gln Gln Leu Thr Phe Gln	
35 40 45 50	
gag tct gtg ctt aaa ctg tgt cag cct gag ctt gag agc agt cag att	249
Glu Ser Val Leu Lys Leu Cys Gln Pro Glu Leu Glu Ser Ser Gln Ile	
55 60 65	
cac ata tca gtg ctg cca atg gag gtc ctg atg tac atc ttc cga tgg	297
His Ile Ser Val Leu Pro Met Glu Val Leu Met Tyr Ile Phe Arg Trp	
70 75 80	
gtg gtg tct agt gac ttg gac ctc aga tca ttg gag cag ttg tcg ctg	345
Val Val Ser Ser Asp Leu Asp Leu Arg Ser Leu Glu Gln Leu Ser Leu	
85 90 95	
gtg tgc aga gga ttc tac atc tgt gcc aga gac cct gaa ata tgg cgt	393
Val Cys Arg Gly Phe Tyr Ile Cys Ala Arg Asp Pro Glu Ile Trp Arg	
100 105 110	
ctg gcc tgc ttg aaa gtt tgg ggc aga agc tgt att aaa ctt gtt ccg	441
Leu Ala Cys Leu Lys Val Trp Gly Arg Ser Cys Ile Lys Leu Val Pro	
115 120 125 130	
tac acg tcc tgg aga gag atg ttt tta gaa cgg cct cgt gtt cgg ttt	489
Tyr Thr Ser Trp Arg Glu Met Phe Leu Glu Arg Pro Arg Val Arg Phe	
135 140 145	
gat ggc gtg tat atc agt aaa acc aca tat att cgt caa ggg gaa cag	537
Asp Gly Val Tyr Ile Ser Lys Thr Thr Tyr Ile Arg Gln Gly Glu Gln	
150 155 160	
tct ctt gat ggt ttc tat aga gcc tgg cac caa gtg gaa tat tac agg	585
Ser Leu Asp Gly Phe Tyr Arg Ala Trp His Gln Val Glu Tyr Tyr Arg	
165 170 175	
tac ata aga ttc ttt cct gat ggc cat gtg atg atg ttg aca acc cct	633
Tyr Ile Arg Phe Phe Pro Asp Gly His Val Met Met Leu Thr Thr Pro	
180 185 190	
gaa gag cct cag tcc att gtt cca cgt tta aga act agg aat acc agg	681
Glu Glu Pro Gln Ser Ile Val Pro Arg Leu Arg Thr Arg Asn Thr Arg	
195 200 205 210	
act gat gca att cta ctg ggt cac tat cgc ttg tca caa gac aca gac	729
Thr Asp Ala Ile Leu Leu Gly His Tyr Arg Leu Ser Gln Asp Thr Asp	
215 220 225	
aat cag acc aaa gta ttt gct gta ata act aag aaa aaa gaa gaa aaa	777
Asn Gln Thr Lys Val Phe Ala Val Ile Thr Lys Lys Lys Glu Glu Lys	
230 235 240	


```

cca ctt gac tat aaa tac aga tat ttt cgt cgt gtc cct gta caa gaa 825
Pro Leu Asp Tyr Lys Tyr Arg Tyr Phe Arg Arg Val Pro Val Gln Glu
      245                      250                      255

gca gat cag agt ttt cat gtg ggg cta cag cta tgt tcc agt ggt cac 873
Ala Asp Gln Ser Phe His Val Gly Leu Gln Leu Cys Ser Ser Gly His
      260                      265                      270

cag agg ttc aac aaa ctc atc tgg ata cat cat tct tgt cac att act 921
Gln Arg Phe Asn Lys Leu Ile Trp Ile His His Ser Cys His Ile Thr
      275                      280                      285                      290

tac aaa tca act ggt gag act gca gtc agt gct ttt gag att gac aag 969
Tyr Lys Ser Thr Gly Glu Thr Ala Val Ser Ala Phe Glu Ile Asp Lys
      295                      300                      305

atg tac acc ccc ttg ttc ttc gcc aga gta agg agc tac aca gct ttc 1017
Met Tyr Thr Pro Leu Phe Phe Ala Arg Val Arg Ser Tyr Thr Ala Phe
      310                      315                      320

tca gaa agg cct ctg tagagcctca agtccagtcc tctatcactt ttgcatgaat 1072
Ser Glu Arg Pro Leu
      325

taa 1075

<210> 12
<211> 327
<212> PRT
<213> Homo sapien

<400> 12
Met Gln Leu Val Pro Asp Ile Glu Phe Lys Ile Thr Tyr Thr Arg Ser
 1      5      10      15
Pro Asp Gly Asp Gly Val Gly Asn Ser Tyr Ile Glu Asp Asn Asp Asp
      20      25      30
Asp Ser Lys Met Ala Asp Leu Leu Ser Tyr Phe Gln Gln Gln Leu Thr
      35      40      45
Phe Gln Glu Ser Val Leu Lys Leu Cys Gln Pro Glu Leu Glu Ser Ser
      50      55      60
Gln Ile His Ile Ser Val Leu Pro Met Glu Val Leu Met Tyr Ile Phe
      65      70      75      80
Arg Trp Val Val Ser Ser Asp Leu Asp Leu Arg Ser Leu Glu Gln Leu
      85      90      95
Ser Leu Val Cys Arg Gly Phe Tyr Ile Cys Ala Arg Asp Pro Glu Ile
      100      105      110
Trp Arg Leu Ala Cys Leu Lys Val Trp Gly Arg Ser Cys Ile Lys Leu
      115      120      125
Val Pro Tyr Thr Ser Trp Arg Glu Met Phe Leu Glu Arg Pro Arg Val
      130      135      140
Arg Phe Asp Gly Val Tyr Ile Ser Lys Thr Thr Tyr Ile Arg Gln Gly
      145      150      155      160
Glu Gln Ser Leu Asp Gly Phe Tyr Arg Ala Trp His Gln Val Glu Tyr

```

[illegible]

```
<210> 13
<211> 2037
<212> DNA
<213> Homo sapien
```

```
<220>  
<221> CDS  
<222> (70) ... (1410)
```

```
<400> 13
aagcaggcag gttgctcagc tgcccccgga gcggttcctc cacctgaggc agactccacg 60
tcggctggc atg agc cgg cgc ccc tgc agc tgc gcc cta cgg cca ccc cgc 111
    Met Ser Arg Arg Pro Cys Ser Cys Ala Leu Arg Pro Pro Arg
        1             5             10
```

tgc	tcc	tgc	agc	gcc	agc	ccc	agc	gca	gtg	aca	gcc	gcc	ggg	cgc	cct	159
Cys	Ser	Cys	Ser	Ala	Ser	Pro	Ser	Ala	Val	Thr	Ala	Ala	Gly	Arg	Pro	
15					20					25					30	

cga ccc tcg gat agt tgt aaa gaa gaa agt tct acc ctt tct gtc aaa 207
Arg Pro Ser Asp Ser Cys Lys Glu Glu Ser Ser Thr Leu Ser Val Lys
 35 40 45

atg aag tgt gat ttt aat tgt aac cat gtt cat tcc gga ctt aaa ctg 255
Met Lys Cys Asp Phe Asn Cys Asn His Val His Ser Gly Leu Lys Leu
50 55 60

gta aaa cct gat gac att gga aga cta gtt tcc tac acc cct gca tat 303
Val Lys Pro Asp Asp Ile Gly Arg Leu Val Ser Tyr Thr Pro Ala Tyr
65 70 75

ttg gaa ggt tcc tgt aaa gac tgc att aaa gac tat gaa agg ctg tca	351
Leu Glu Gly Ser Cys Lys Asp Cys Ile Lys Asp Tyr Glu Arg Leu Ser	
80 85 90	
tgt att ggg tca ccg att gtg agc cct agg att gta aaa ctt gaa act	399
Cys Ile Gly Ser Pro Ile Val Ser Pro Arg Ile Val Lys Leu Glu Thr	
95 100 105 110	
gaa agc aag cgc ttg cat aac aag gaa aat caa cat gtg caa cag aca	447
Glu Ser Lys Arg Leu His Asn Lys Glu Asn Gln His Val Gln Gln Thr	
115 120 125	
ctt aat agt aca aat gaa ata gaa gca cta gag acc agt aga ctt tat	495
Leu Asn Ser Thr Asn Glu Ile Glu Ala Leu Glu Thr Ser Arg Leu Tyr	
130 135 140	
gaa gac agt ggc tat tcc tca ttt tct cta caa agt ggc ctc agt gaa	543
Glu Asp Ser Gly Tyr Ser Ser Phe Ser Leu Gln Ser Gly Leu Ser Glu	
145 150 155	
cat gaa gaa ggt acc ctc ctg gag gag aat ttc ggt gac agt cta caa	591
His Glu Glu Gly Thr Leu Leu Glu Glu Asn Phe Gly Asp Ser Leu Gln	
160 165 170	
tcc tgc ctg cta caa ata caa agc cca gac caa tat ccc aac aaa aac	639
Ser Cys Leu Leu Gln Ile Gln Ser Pro Asp Gln Tyr Pro Asn Lys Asn	
175 180 185 190	
ttg ctg cca gtt ctt cat ttt gaa aaa gtg gtt tgt tca aca tta aaa	687
Leu Leu Pro Val Leu His Phe Glu Lys Val Val Cys Ser Thr Leu Lys	
195 200 205	
aag aat gca aaa cga aat cct aaa gta gat cgg gag atg ctg aag gaa	735
Lys Asn Ala Lys Arg Asn Pro Lys Val Asp Arg Glu Met Leu Lys Glu	
210 215 220	
att ata gcc aga gga aat ttt aga ctg cag aat ata att ggc aga aaa	783
Ile Ile Ala Arg Gly Asn Phe Arg Leu Gln Asn Ile Ile Gly Arg Lys	
225 230 235	
atg ggc cta gaa tgt gta gat att ctc agc gaa ctc ttt cga agg gga	831
Met Gly Leu Glu Cys Val Asp Ile Leu Ser Glu Leu Phe Arg Arg Gly	
240 245 250	
ctc aga cat gtc tta gca act att tta gca caa ctc agt gac atg gac	879
Leu Arg His Val Leu Ala Thr Ile Leu Ala Gln Leu Ser Asp Met Asp	
255 260 265 270	
tta atc aat gtg tct aaa gtg agc aca act tgg aag aag atc cta gaa	927
Leu Ile Asn Val Ser Lys Val Ser Thr Thr Trp Lys Lys Ile Leu Glu	
275 280 285	

gat gat aag ggg gca ttc cag ttg tac agt aaa gca ata caa aga gtt 975
Asp Asp Lys Gly Ala Phe Gln Leu Tyr Ser Lys Ala Ile Gln Arg Val
290 295 300

acc gaa aac aac aat aaa ttt tca cct cat gct tca acc aga gaa tat 1023
Thr Glu Asn Asn Lys Phe Ser Pro His Ala Ser Thr Arg Glu Tyr
305 310 315

gtt atg ttc aga acc cca ctg gct tct gtt cag aaa tca gca gcc cag 1071
Val Met Phe Arg Thr Pro Leu Ala Ser Val Gln Lys Ser Ala Ala Gln
320 325 330

act tct ctc aaa aaa gat gct caa acc aag tta tcc aat caa ggt gat 1119
Thr Ser Leu Lys Lys Asp Ala Gln Thr Lys Leu Ser Asn Gln Gly Asp
335 340 345 350

cag aaa ggt tct act tat agt cga cac aat gaa ttc tct gag gtt gcc 1167
Gln Lys Gly Ser Thr Tyr Ser Arg His Asn Glu Phe Ser Glu Val Ala
355 360 365

aag aca ttg aaa aag aac gaa agc ctc aaa gcc tgt att cgc tgt aat 1215
Lys Thr Leu Lys Lys Asn Glu Ser Leu Lys Ala Cys Ile Arg Cys Asn
370 375 380

tca cct gca aaa tat gat tgc tat tta caa cgg gca acc tgc aaa cga 1263
Ser Pro Ala Lys Tyr Asp Cys Tyr Leu Gln Arg Ala Thr Cys Lys Arg
385 390 395

gaa ggc tgt gga ttt gat tat tgt acg aag tgt ctc tgt aat tat cat 1311
Glu Gly Cys Gly Phe Asp Tyr Cys Thr Lys Cys Leu Cys Asn Tyr His
400 405 410

act act aaa gac tgt tca gat ggc aag ctc ctc aaa gcc agt tgt aaa 1359
Thr Thr Lys Asp Cys Ser Asp Gly Lys Leu Leu Lys Ala Ser Cys Lys
415 420 425 430

ata ggt ccc ctg cct ggt aca aag aaa agc aaa aag aat tta cga aga 1407
Ile Gly Pro Leu Pro Gly Thr Lys Lys Ser Lys Lys Asn Leu Arg Arg
435 440 445

ttg tgatctctta ttaaataaat tggtactgat catgaatggt agttagaaaa 1460
Leu

tgtagggttt taacttaaaa aaaattgtat tgtgattttc aattttatgt tgaaatcggt 1520
gtagtatcct gaggtttttt tccccccaga agataaagag gatagacaac ctcttaaaat 1580
atttttacaa tttaatgaga aaaagttaa aattctcaat acaaatacaa caatttaaat 1640
attttaagaa aaaaggaaaa gtagatagtg atactgaggg taataaaaaa ttgattcaat 1700
tttatggtaa aggaaaccca tgcaatttta cctagacagt cttaaataatg tctgggttttc 1760
catctgttag catttcagac attttatgtt cctcttactc aattgatacc aacagaaata 1820
tcaacttctg gagtctatta aatgtgttgt cacctttcta aagctttttt tcattgtgtg 1880
tatttcccaa gaaagtatcc ttgttaaaaa cttgcttggtt ttccttattt ctgaaatctg 1940
ttttaatatatt ttgtatata tgtaaatatt tctgtatttt ttatatgtca aagaatatgt 2000

ctcttgatg tacatataaa aataaatttt gctcaat

2037

<210> 14
<211> 447
<212> PRT
<213> Homo sapien

<400> 14
Met Ser Arg Arg Pro Cys Ser Cys Ala Leu Arg Pro Pro Arg Cys Ser
1 5 10 15
Cys Ser Ala Ser Pro Ser Ala Val Thr Ala Ala Gly Arg Pro Arg Pro
20 25 30
Ser Asp Ser Cys Lys Glu Glu Ser Thr Leu Ser Val Lys Met Lys
35 40 45
Cys Asp Phe Asn Cys Asn His Val His Ser Gly Leu Lys Leu Val Lys
50 55 60
Pro Asp Asp Ile Gly Arg Leu Val Ser Tyr Thr Pro Ala Tyr Leu Glu
65 70 75 80
Gly Ser Cys Lys Asp Cys Ile Lys Asp Tyr Glu Arg Leu Ser Cys Ile
85 90 95
Gly Ser Pro Ile Val Ser Pro Arg Ile Val Lys Leu Glu Thr Glu Ser
100 105 110
Lys Arg Leu His Asn Lys Glu Asn Gln His Val Gln Gln Thr Leu Asn
115 120 125
Ser Thr Asn Glu Ile Glu Ala Leu Glu Thr Ser Arg Leu Tyr Glu Asp
130 135 140
Ser Gly Tyr Ser Ser Phe Ser Leu Gln Ser Gly Leu Ser Glu His Glu
145 150 155 160
Glu Gly Thr Leu Leu Glu Glu Asn Phe Gly Asp Ser Leu Gln Ser Cys
165 170 175
Leu Leu Gln Ile Gln Ser Pro Asp Gln Tyr Pro Asn Lys Asn Leu Leu
180 185 190
Pro Val Leu His Phe Glu Lys Val Val Cys Ser Thr Leu Lys Lys Asn
195 200 205
Ala Lys Arg Asn Pro Lys Val Asp Arg Glu Met Leu Lys Glu Ile Ile
210 215 220
Ala Arg Gly Asn Phe Arg Leu Gln Asn Ile Ile Gly Arg Lys Met Gly
225 230 235 240
Leu Glu Cys Val Asp Ile Leu Ser Glu Leu Phe Arg Arg Gly Leu Arg
245 250 255
His Val Leu Ala Thr Ile Leu Ala Gln Leu Ser Asp Met Asp Leu Ile
260 265 270
Asn Val Ser Lys Val Ser Thr Thr Trp Lys Lys Ile Leu Glu Asp Asp
275 280 285
Lys Gly Ala Phe Gln Leu Tyr Ser Lys Ala Ile Gln Arg Val Thr Glu
290 295 300
Asn Asn Asn Lys Phe Ser Pro His Ala Ser Thr Arg Glu Tyr Val Met
305 310 315 320
Phe Arg Thr Pro Leu Ala Ser Val Gln Lys Ser Ala Ala Gln Thr Ser
325 330 335
Leu Lys Lys Asp Ala Gln Thr Lys Leu Ser Asn Gln Gly Asp Gln Lys
340 345 350
Gly Ser Thr Tyr Ser Arg His Asn Glu Phe Ser Glu Val Ala Lys Thr

355		360		365
Leu Lys Lys Asn Glu Ser	Leu Lys Ala Cys Ile Arg Cys Asn Ser Pro			
370	375	380		
Ala Lys Tyr Asp Cys Tyr	Leu Gln Arg Ala Thr Cys Lys Arg Glu Gly			
385	390	395		400
Cys Gly Phe Asp Tyr Cys Thr	Lys Cys Leu Cys Asn Tyr His Thr Thr			
	405	410		415
Lys Asp Cys Ser Asp Gly Lys	Leu Leu Lys Ala Ser Cys Lys Ile Gly			
	420	425		430
Pro Leu Pro Gly Thr Lys Lys	Ser Lys Lys Asn Leu Arg Arg Leu			
	435	440		445

<210> 15
 <211> 20
 <212> PRT
 <213> Homo sapien

<400> 15
 Ser Glu Ser Pro Gly Ala Leu Arg Ser Gly Ser Leu Arg Cys Ile Ser
 1 5 10 15
 Leu Arg Ile Cys
 20

<210> 16
 <211> 20
 <212> PRT
 <213> Homo sapien

<400> 16
 Val Cys Arg Gly Arg Ile Arg Ser Gly Ser Leu Arg Cys Ile Ser Leu
 1 5 10 15
 Arg Ile Cys Arg
 20

<210> 17
 <211> 20
 <212> PRT
 <213> Homo sapien

<400> 17
 Leu Leu Arg Leu Gly Cys Ile Arg Leu Leu Met Leu Arg Arg Gly Val
 1 5 10 15
 Val Phe Arg Leu
 20

<210> 18
 <211> 20
 <212> PRT
 <213> Homo sapien

```
<210> 19
<211> 20
<212> PRT
<213> Homo sapien
```

```
<210> 20
<211> 20
<212> PRT
<213> Homo sapien
```

```
<210> 21
<211> 20
<212> PRT
<213> Homo sapien
```

```
<210> 22
<211> 20
<212> PRT
<213> Homo sapien
```

```
<400> 22
Ser Leu Gly Leu Ser Val Cys Ile Gly Arg Arg Ala Gly Gly Gly Phe
 1             5             10             15
Arg Gly Phe Gly
```

20

<210> 23
<211> 20
<212> PRT
<213> Homo sapien

<400> 23
Arg Phe Ala Leu Ser Ile Gly Val Cys Val Val Val Arg Val Gly Ile
1 5 10 15
Cys Leu Gly Met
20

<210> 24
<211> 20
<212> PRT
<213> Homo sapien

<400> 24
Ser Ala Val Leu Val Leu Val Tyr Val Ser Ala Ala Leu Arg Gly Arg
1 5 10 15
Gly Phe Gly Ile
20

<210> 25
<211> 20
<212> PRT
<213> Homo sapien

<400> 25
His Gly Gly Gly Arg Gly Ala Leu Val Ser Val Met Tyr Leu Cys Gly
1 5 10 15
Phe Ile Arg Leu
20

<210> 26
<211> 18
<212> PRT
<213> Homo sapien

<400> 26
Arg Gly Arg Val Ile Gly Met Trp Val Gly Leu Arg Cys Arg Met Phe
1 5 10 15
Leu Val

<210> 27
<211> 15

<212> PRT

<213> Homo sapien

<400> 27

Val	Asp	Trp	Ala	Val	Tyr	Ser	Val	Val	Trp	Arg	Tyr	Thr	Thr	Thr
1				5					10					15

<210> 28

<211> 20

<212> PRT

<213> Homo sapien

<400> 28

Lys	Thr	Ser	Val	Ile	Leu	Val	Trp	Arg	Leu	Ser	Leu	Phe	Phe	Cys	Leu
1				5					10					15	
Tyr	Arg	Ser	Leu												
			20												

<210> 29

<211> 7

<212> PRT

<213> Homo sapien

<400> 29

Ala	Asn	Arg	Cys	Trp	Arg	Glu
1				5		

<210> 30

<211> 13

<212> PRT

<213> Homo sapien

<400> 30

Glu	Gly	Thr	Leu	Ser	Lys	Arg	Met	Trp	Arg	Thr	His	Asn
1				5					10			

<210> 31

<211> 10

<212> PRT

<213> Homo sapien

<400> 31

Ser	Trp	Arg	Asp	Met	Thr	Gln	Ser	Gly	Met
1				5					10

<210> 32

<211> 11

<212> PRT

<213> Homo sapien

<400> 32

Asp Val Pro Trp Gln Arg Ala Cys Ala Arg Gln
1 5 10

<210> 33

<211> 9

<212> PRT

<213> Homo sapien

<400> 33

Leu Glu Arg Val Ala Arg Trp Val Leu
1 5

<210> 34

<211> 12

<212> PRT

<213> Homo sapien

<400> 34

Val Ala Asp Val Leu Val Phe Trp Gly Tyr Val Phe
1 5 10

<210> 35

<211> 8

<212> PRT

<213> Homo sapien

<400> 35

Gly Asp Val Gly Val Phe Pro Glu
1 5

<210> 36

<211> 16

<212> PRT

<213> Homo sapien

<220>

<221> VARIANT

<222> (1)...(16)

<223> Xaa = Any Amino Acid

<400> 36

Pro Glu Met Met Leu Glu Gly Pro Lys Tyr Cys Leu Xaa Leu Xaa Glu
1 5 10 15

<210> 37

<211> 7
<212> PRT
<213> Homo sapien

<400> 37
Leu Leu Tyr Gly Ala Leu Ala
1 5

<210> 38
<211> 11
<212> PRT
<213> Homo sapien

<400> 38
Gly Ala Ile Lys Phe Ala His Glu Ser Cys Glu
1 5 10

<210> 39
<211> 5
<212> PRT
<213> Homo sapien

<400> 39
Pro Met Ala Met Asp
1 5

<210> 40
<211> 5
<212> PRT
<213> Homo sapien

<400> 40
Gln Glu Glu Glu Met
1 5

<210> 41
<211> 12
<212> PRT
<213> Homo sapien

<400> 41
Ile Ser Val Val His Gly Ile Gly Ser Asp Ser Asp
1 5 10

<210> 42
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 42
gggaattcgg acttatggca tgtaaaca 28

<210> 43
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 43
tagccaagtt gcgaatgga 19

<210> 44
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 44
gtgaattcat gcaacttgta cctgatatag agttc 35

<210> 45
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 45
ggactcgagg ctctacagag gcc 23

<210> 46
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 46
gatcaagctt atggcttcag aagagctaca g 31

<210> 47
<211> 37

<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 47
gatcgaattc tccaaattcc gtgtctcctt tggcttg 37

<210> 48
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 48
cctctgaatt ccatatgagc gataaaatta ttcacc 36

<210> 49
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 49
gatcctcgag tagatggcca gctaggccag gtta 34

<210> 50
<211> 497
<212> PRT
<213> Homo sapiens

<400> 50
Met Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Ser Arg Gly Ser Asn
1 5 10 15
Asn Phe Gly Asn Glu Glu Phe Asp Cys His Phe Leu Asp Glu Gly Phe
20 25 30
Thr Ala Lys Asp Ile Leu Asp Gln Lys Ile Asn Glu Val Ser Ser Ser
35 40 45
Asp Asp Lys Asp Ala Phe Tyr Val Ala Asp Leu Gly Asp Ile Leu Lys
50 55 60
Lys His Leu Arg Trp Leu Lys Ala Leu Pro Arg Val Thr Pro Phe Tyr
65 70 75 80
Ala Val Lys Cys Asn Asp Ser Lys Ala Ile Val Lys Thr Leu Ala Ala
85 90 95
Thr Gly Thr Gly Phe Asp Cys Ala Ser Lys Thr Glu Ile Gln Leu Val
100 105 110
Gln Ser Leu Gly Val Pro Pro Glu Arg Ile Ile Tyr Ala Asn Pro Cys
115 120 125

Ser